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FIG. 1A

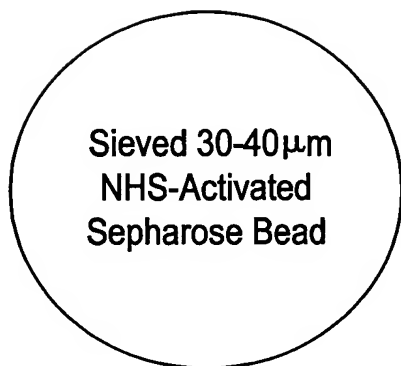


FIG. 1B

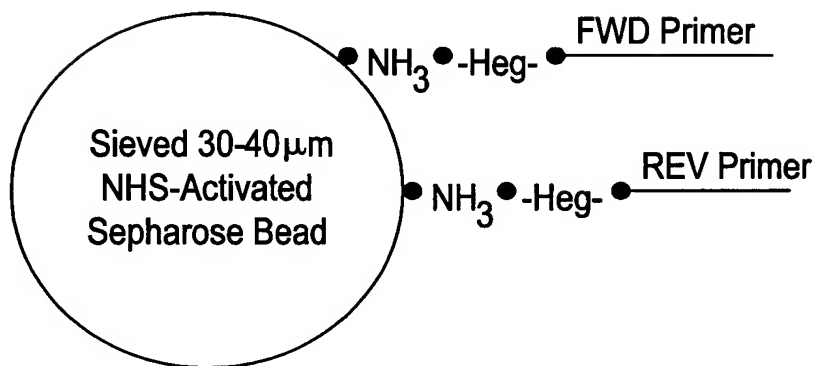


FIG. 1C

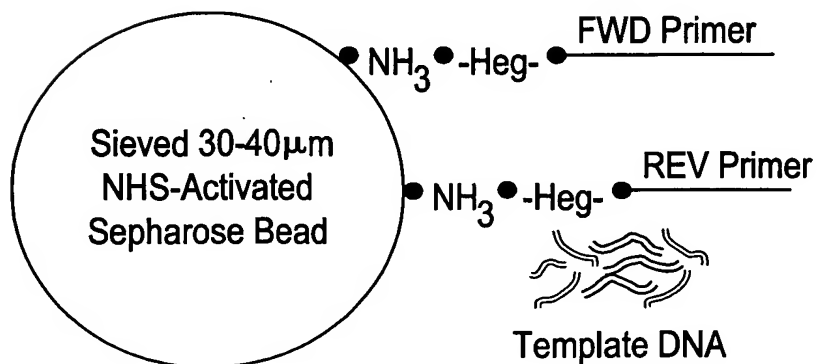


FIG. 1D

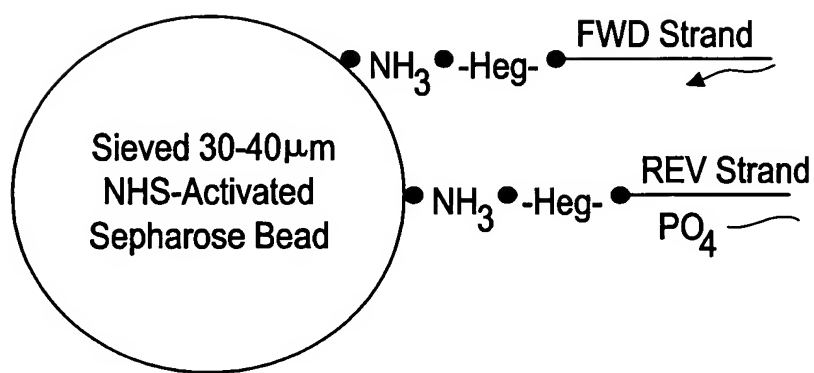


FIG. 1E

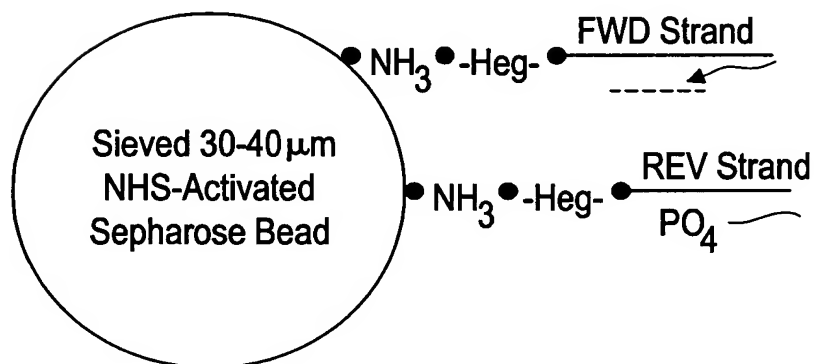


FIG. 1F

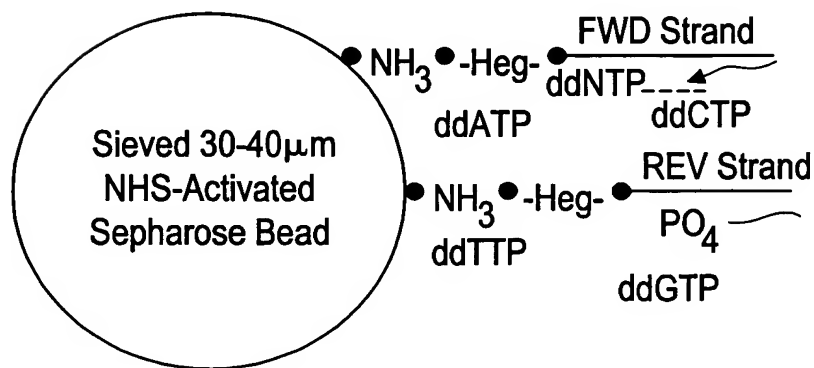


FIG. 1G

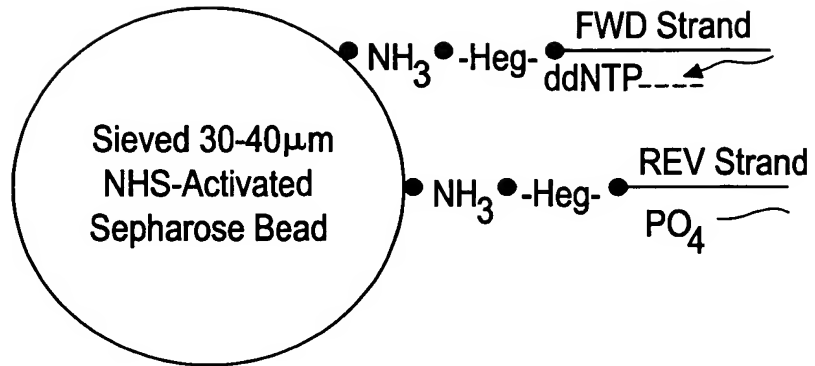


FIG. 1H

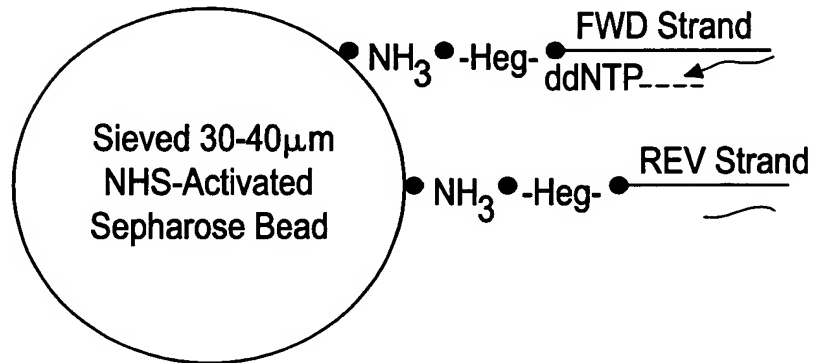


FIG. 1I

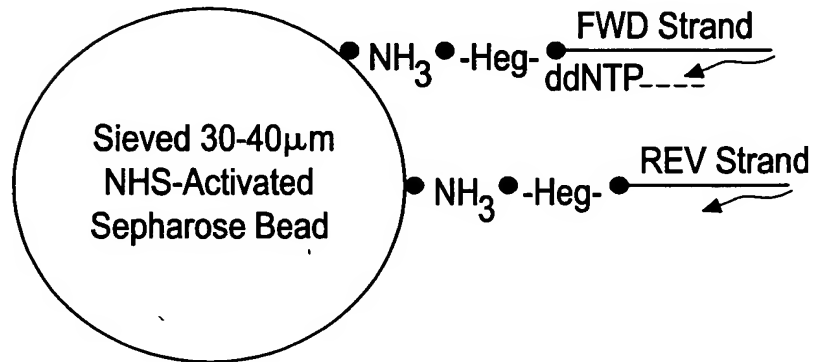


FIG. 1J

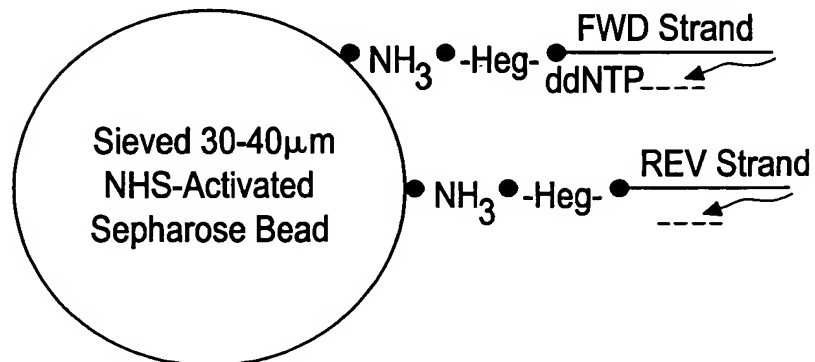
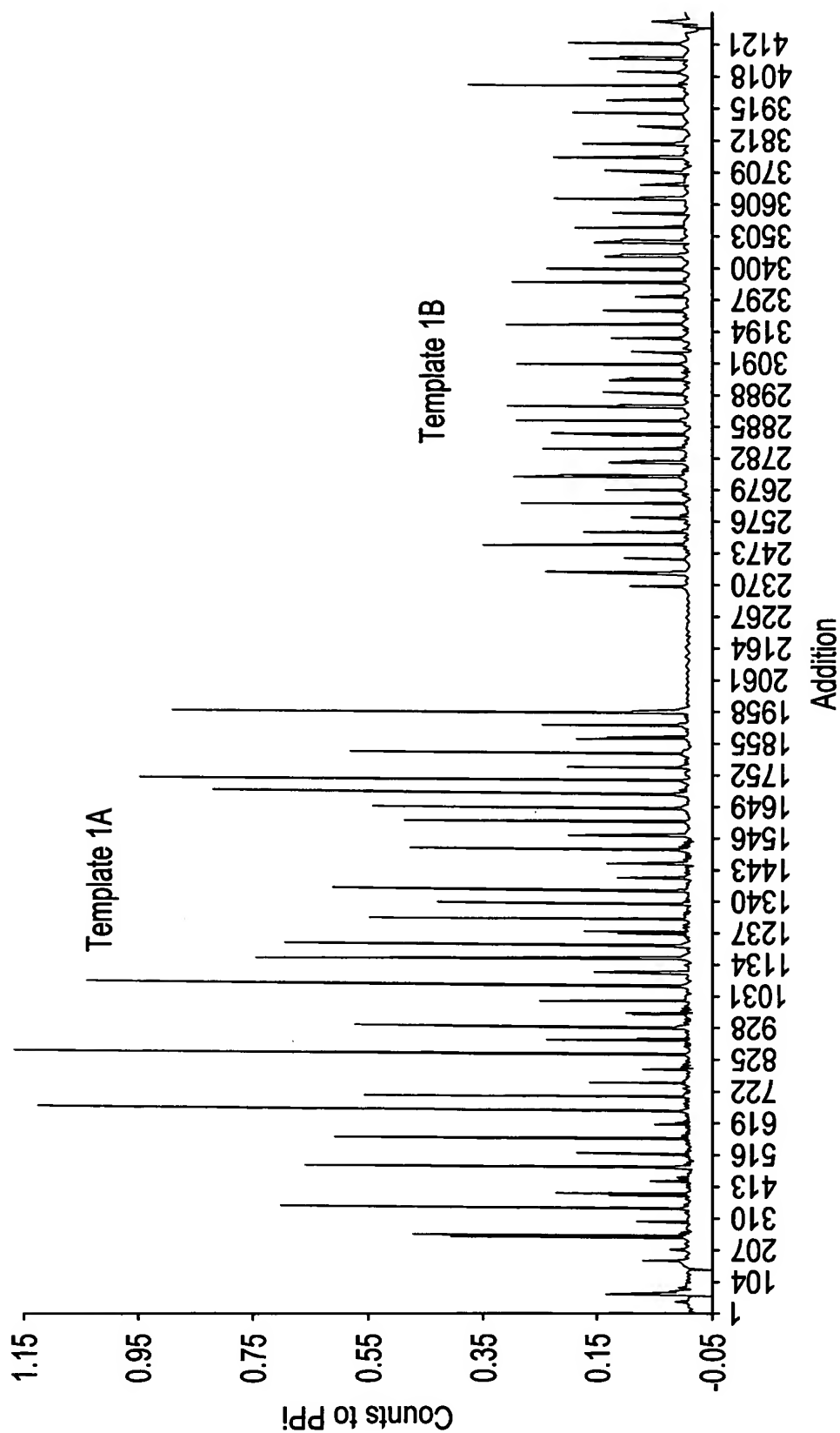
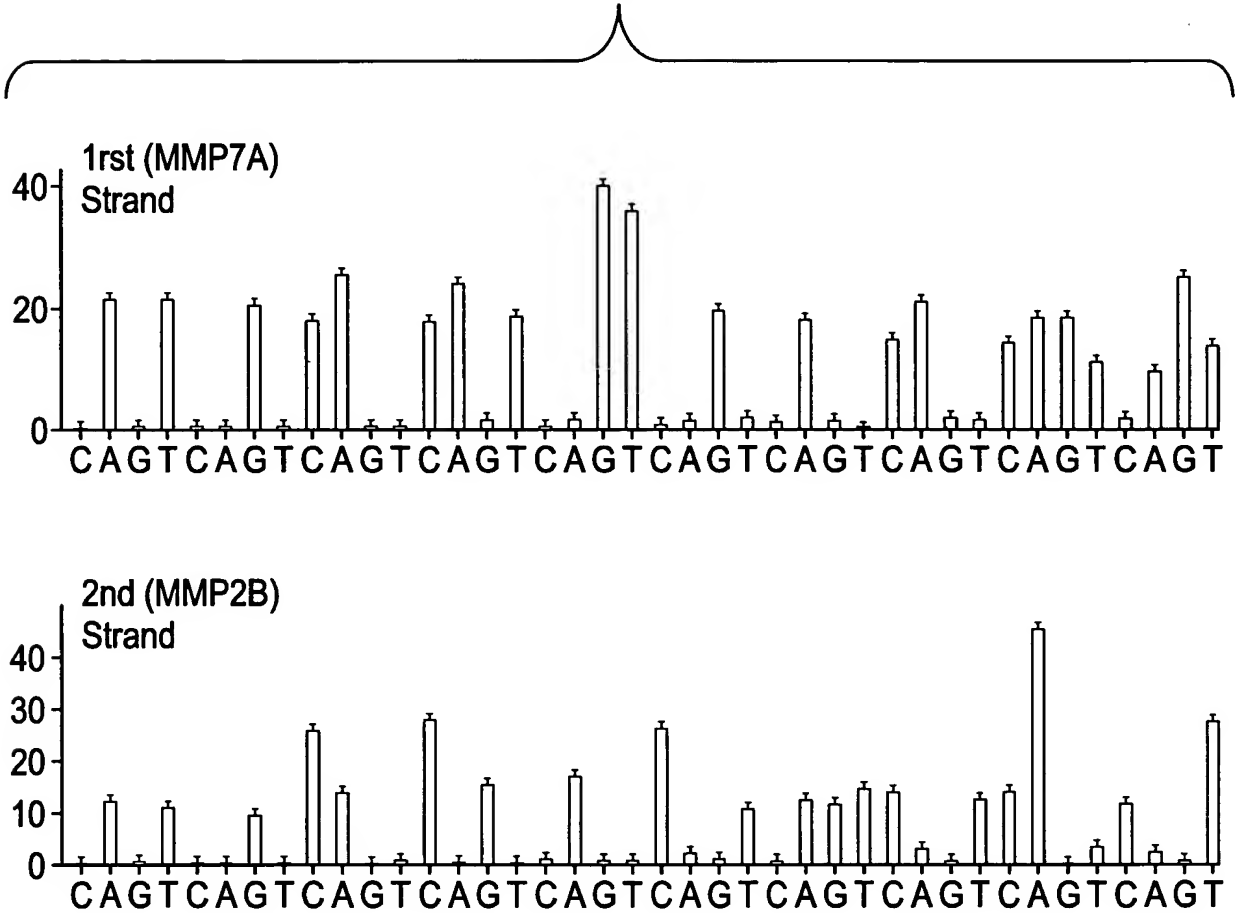


FIG. 2

1_21_03 N7 from 1_14_03 10X Double Strand





Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00001_1362_1660.well	ATGCACATGGTTGACACAGTGGT	22

ATGC ACATGGTTGACACAGTGG

ATGC CACCGACCTAGTCTCAACTT

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00003 1363 1660.well	ATGCCACCGACCTAGTCTCAA	25

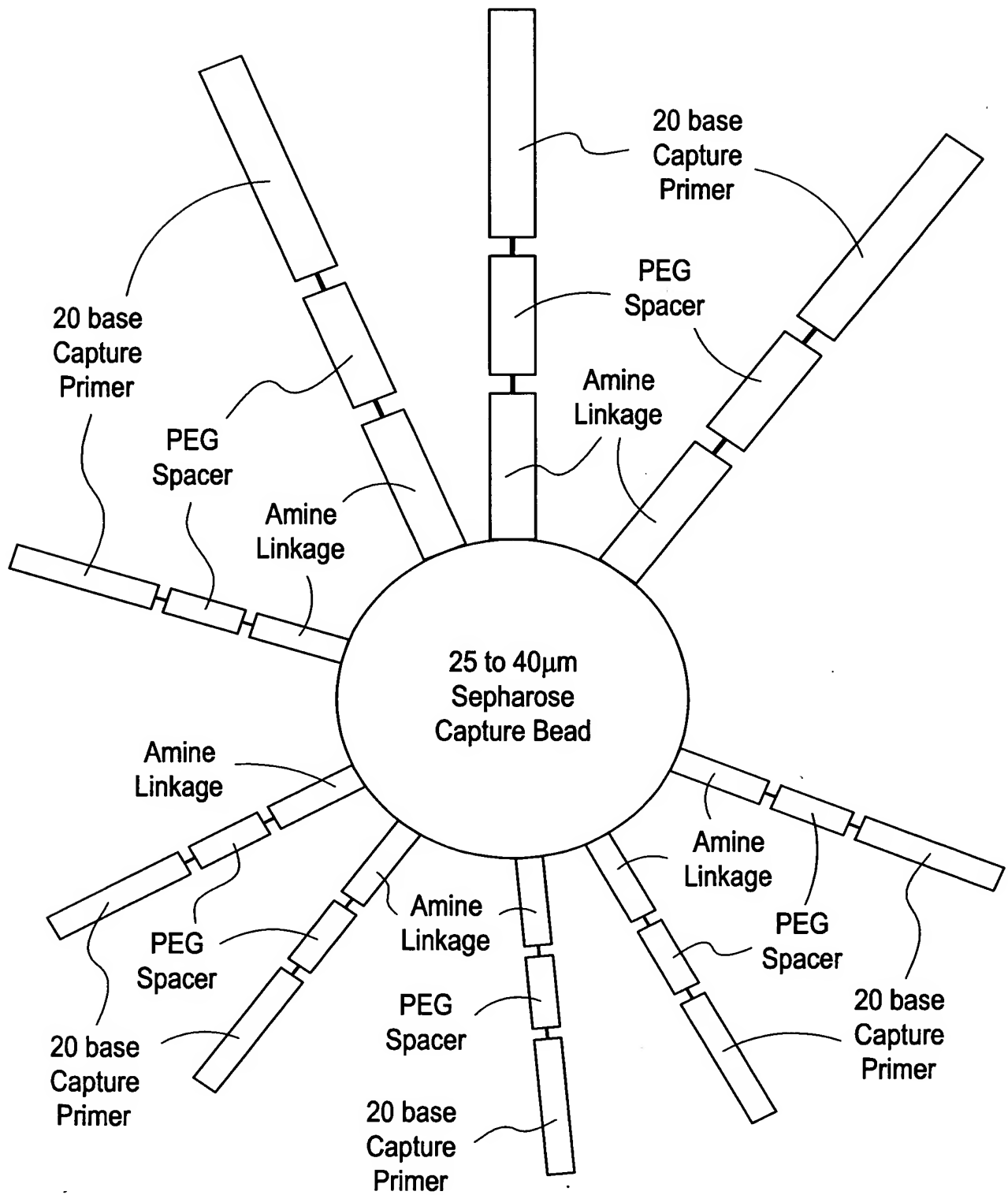
FIG. 4

FIG. 5A

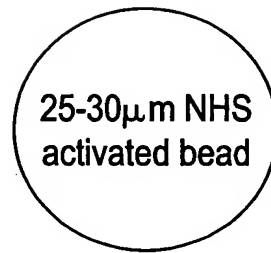


FIG. 5B

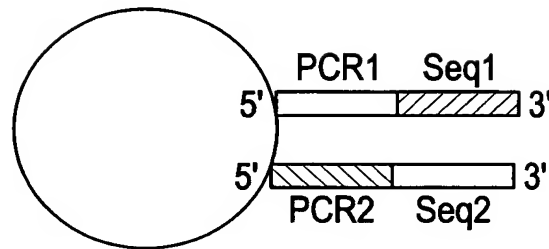


FIG. 5C

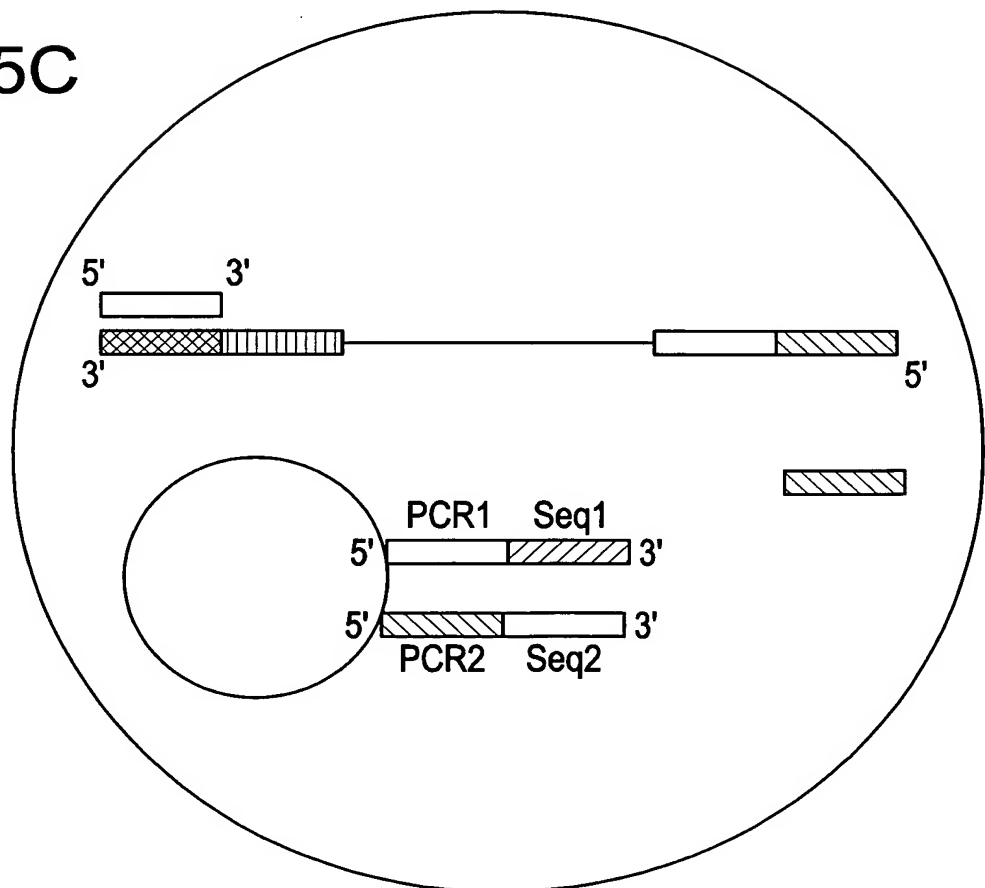


FIG. 6

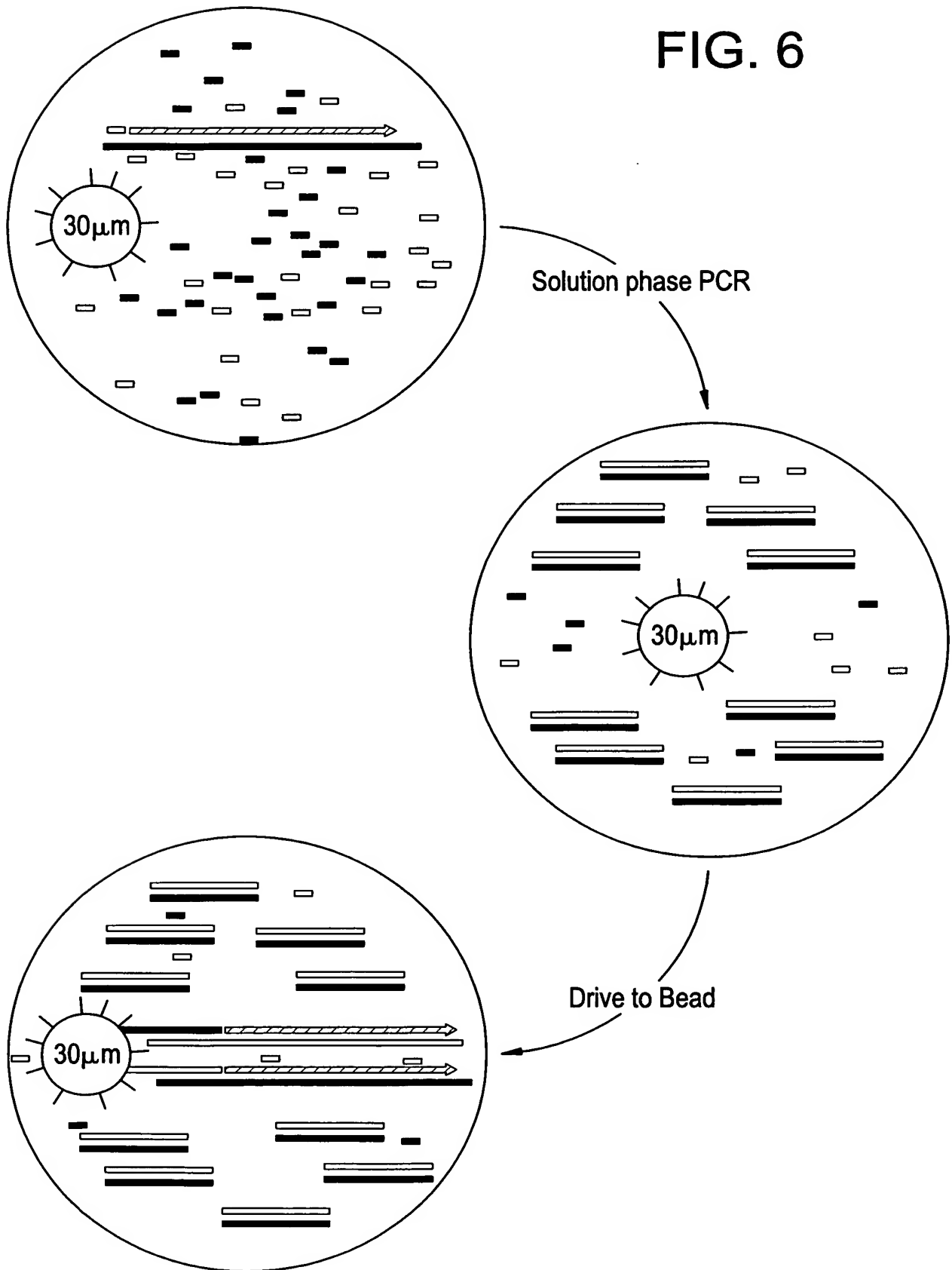


FIG. 7A

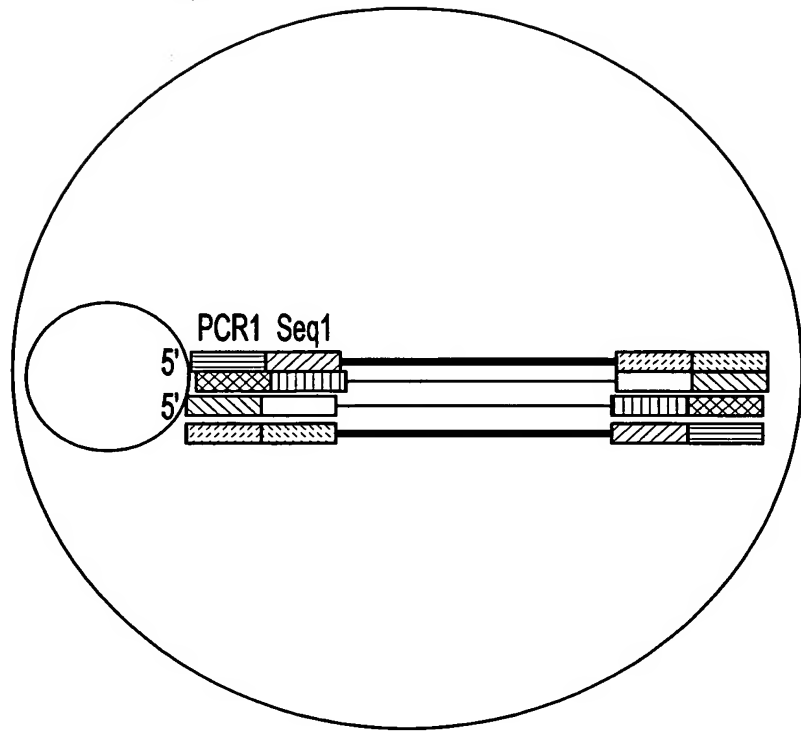


FIG. 7B

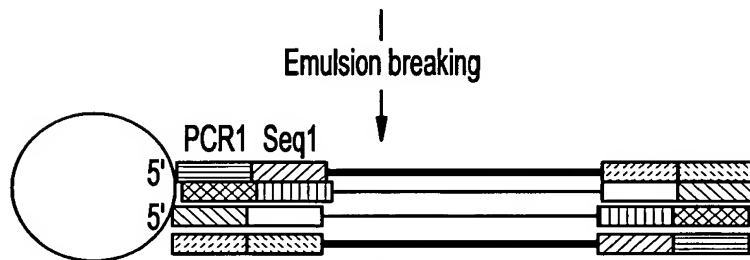


FIG. 7C

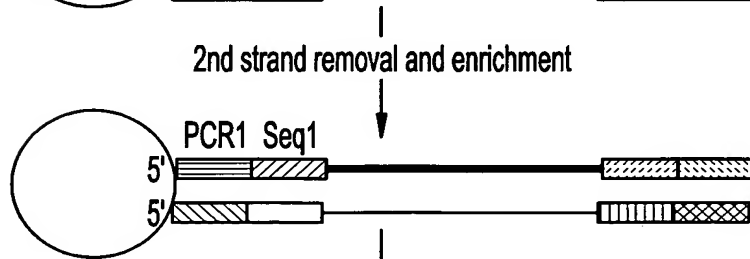


FIG. 7D

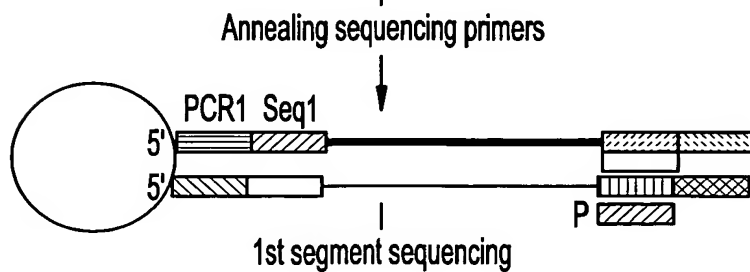


FIG. 7E

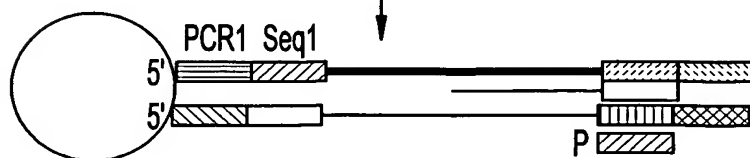
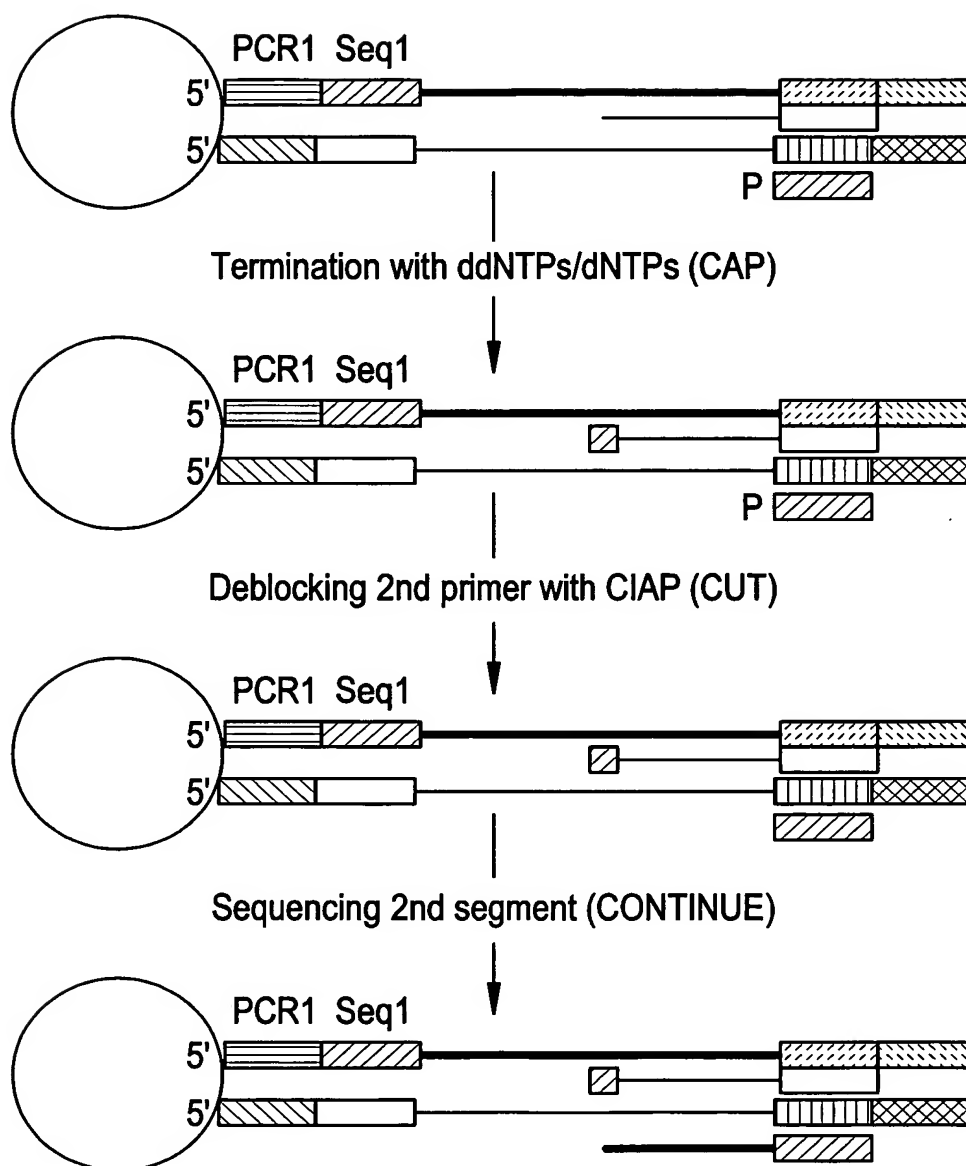


FIG. 8



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FIG. 9A

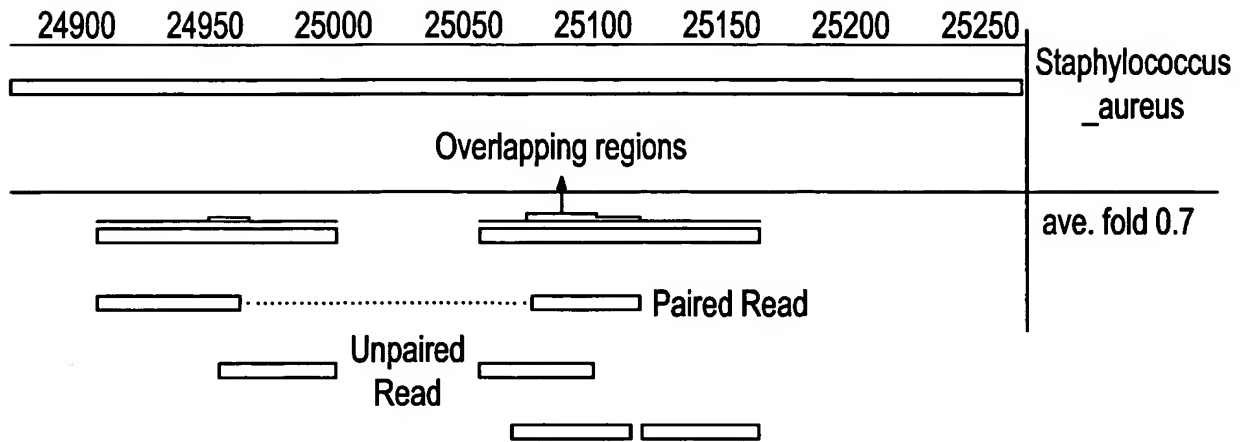
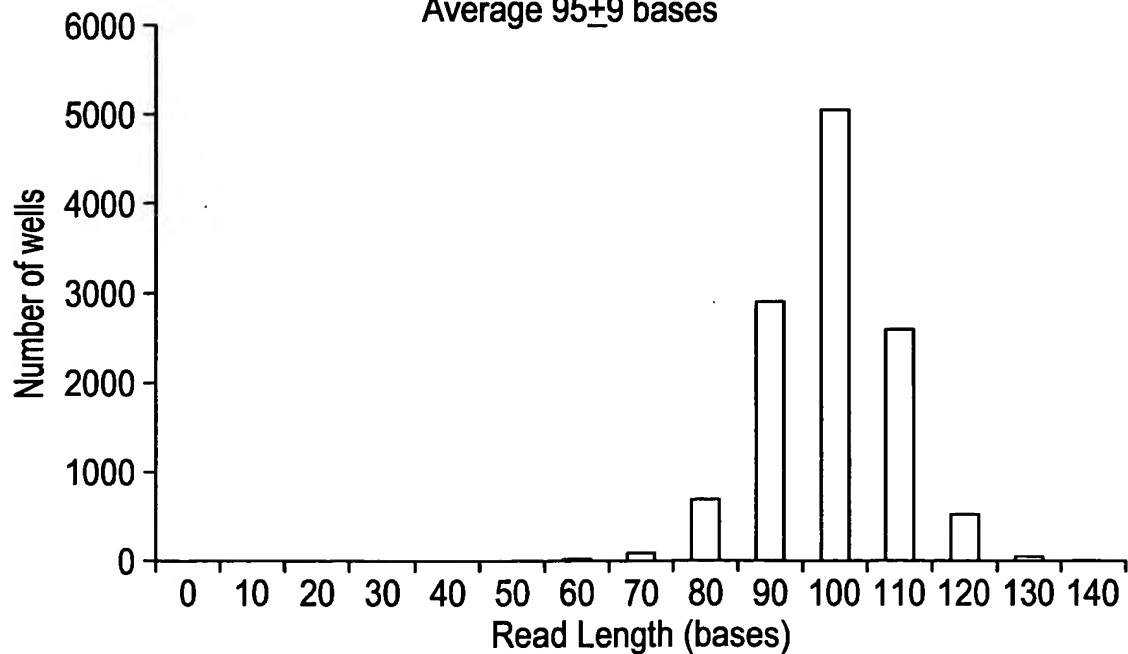


FIG. 9B

Total Reads	31,785
Total 1st Strand	15,770
Total 2nd Strand	16,015
Paired	11,799
Non Paired Reads	8,187
Total Coverage	38%

FIG. 10

Average 95±9 bases



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FIG. 11

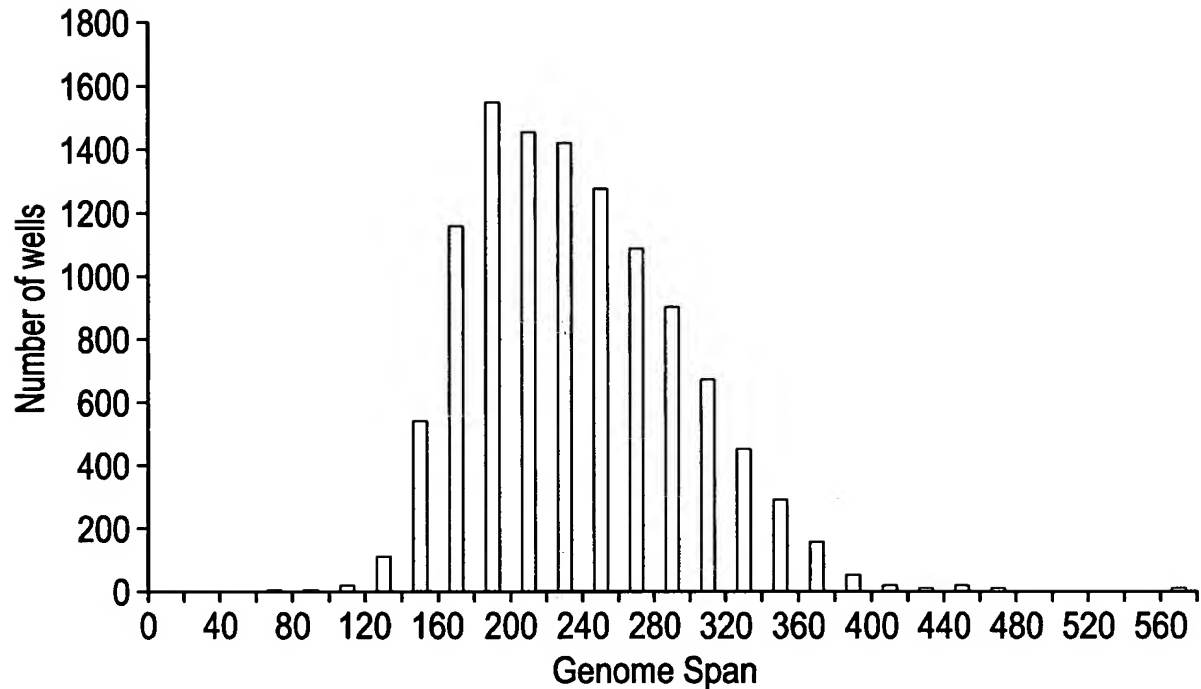


FIG. 12

Well	Genome Position	Orientation	Alignment String
00364_0548_2509	571366	F	TATTGTTGATGCTGTAAAAaGAAGCTACTGGTGTAGtATTTTATGAAGTT
00364_0548_2509_D2	571512	R	TGCTCAAAGAATTCATTTAAAATATGACCATATTTCAATTGTATCTTT
00383_0985_2232	1487890	R	AAGCGAACAGTCAAGTACCACAGTCAGTTGACtTTTACACAAGCGGAT
00383_0985_2232_D2	1487769	F	TACAGGTGTTGGTATGCCATTTGCGATTTGTTGCGCTTGGTTAGCCG
00397_0940_2923	2611033	F	AACATATAAACATCCCCTATCTCAATTTCCGCTTCCATGTaCAAAAAAAGC
00397_0940_2923_D2	2611164	R	TAGATATCACTTGCGTGTTACTGGTAATGCAGGCATGAG
00417_0611_1933	122001	R	ATTCAACTCTGGAAATGCtTTCTTGATACGCCTCGATGATG
00417_0611_1933_D2	121930	F	GATGAGGAGCTGCAATGGCAATGGGTAAAGGCATCATCG
00434_0595_0993	2022591	R	TGTATCTCGATTTGGATTAGTTGCtTTTGCATCTTCATTAGACC
00434_0595_0993_D2	2022473	F	CATTAACATCTGCACCAGAAATAGCTTCTAATACGATTGC
00443_1003_0754	107373	F	GCGACGACGTCCAGCTAATAACGCTGCACCTAAGGCTAATGATAAT
00443_1003_0754_D2	107502	R	AAACCATGCAGATGCTAACAAAGCTCAAGCATTACCAGAACT
00454_1257_3047	59038	R	TGTTGCTGCATCATAATTTAATACTACATCATTTAAITCTTTGG
00454_1257_3047_D2	58880	F	GCAGATGGTGTGACTAACCAAGTTGGTCAAAATGCCCTAAATACAAAAGAT